

100694-121801

Figure 1-A
T. reesei eg16 nucleotide sequence (coding and non-coding)

CCACGGCTCCGAGCAGTGTCTCTCTCTCACTGCTTCGTCAATGAAGGTCTCTCGAGTCTCTTGGCCCTTGTCTCTGGGGGCCCGT
CATCCCTGCCCATGCTGCCCTTTTCATGGAAGAACGTCAAGCTCGGGCGGGCGGCTTCGTCCCCGGCATCATCTTCCA
TCCAAAGACAAAAGGCTAGCATATGCAGAAACAGATATTGGCGGCTGTACCGCTCAACGCCGACGACTCATGACCGC
CGTCACGGATGGGATTGCTGATAATGCCGCTGGCAAACTGGGCGATCGACGCTGTTGCGCTTGATCCGCAGGACGATCA
AAAGGTGATGCCGAGTCCGCGATGGCATGTATACGAACAGCTGGGATCCGAGTAATGGAGCCATCATTCGCTCGTCAGACCGCGG
CGAAACGTGTCCTTCAACCAACTTGCCCTTCAAAGTCGGGGTTAAATGCCAGGACCGGAGCCGGAGAGCGTCTGGCTGT
CGATCCGGCCAACTCCAACATCATCTACTTTTGGTGCTCGCTCAGGAAACGGCCCTCTGGAAGTCTACGGACGGCGGTGAC
CTTTTCCAAGGTCTCGTCTGTTACGGCAACTGGGACGTACATCCCAGACCCGAGTGATTC AACGGCTACAAACAGCGACAA
GCAAGGACTCATGTGGTTACGTTTCGACTCAACCCAGCAGCACGACCGGGGAGCCACGCTCTCGTATCTTTTGTGGCACGGC
TGATAACATCATCTGCTTTCAGTCTATGTAGCACGAATGCCGCTCCACGTGGAGTCTGTACCGGGCGAGCCAGGAAATA
CTTTCTCAAGCGGAAACTGCAGCCAGCAGAGAAAGCCCTTGTTATCTGACCTATTCCGATGGCACAGGCGCTATGATGG
CACACTGGCTCAGTGTGGAGGTACGACATTGCAGGGGGAACTTGGAAAGACATCACCCCTGTCTCTGGATCAGATCTATA
CTTTGGCTTTGGCGGCTTGGCCTCGATTTCGAAAGCCAGGAACCTTGTGTGCTTCTTTGAACTCTTGGTGGCCAGA
TGCTCAGCTGTTTCGGTCGACCGACTCTGGGACAAACATGGAGCCCGATCTGGCGGTGGCGGAGCTATCCGACTGAGACCTA
TTACTACAGCATCTCAACTCCCAAGCACCGTGATCAAGAACAACTTTATCGATGTGACGAGCGAGTCACCGTCCGATGG
TCTCATCAAGCGCCTCGGCTGGATGATTGAGTCTCTCGAGATTGACCCAAACCGACAGCAACCACTGGCTCTACGGCACCGG
AATGACAACTTTTGGCGGCCACGATCTCACCAACTGGGACACGCGCCACAATGTGTCAATCCAATCACTGGCAGACGGCAT
CGAGGAATTCTCCGTCAGGACCTGGCCTCTGCACCCGGCGGAAGCGAGCTATTGGCCGCGAGTTCGGAGACGACAAACGGCTT
CACCTTTGCCAGCAGAAACGACCTCGGGACATCGCCGCAGACGGTCTGGGCAACGCCACATGGGCCACCTCGACGAGCGT
CGACTACGCCGGGAACCTCGGTCAAGAGCGTCTCGCGTCGGCAACACCGCCGCAACGCAACAGGTGGCCATCTCGTCCGA
CGCGGGCGGACGTGGAGCATCGACTACCGGGCCGACACGTCCATGAACGGCGGCACGGTGGCCCTATTGGGCCGACGGCGA
CACGATCCTCTGGTCGACCGCCTCGTCCGGCGTGCAAGCGCTCGCAGTTCCAGGCGAGCTTTGCCCTCGTCTCGAGCCTGCC
CGCGGGCGCGTCATCGCCTCGGACAAAGAACCAACAGCGTCTTCTACGCCGCTCCGGATCGACCTTTTACGTACGCA
GGACACCGGCAGCAGCTTCACGCGGGGCCCAAGCTGGGCAGCGCAGGACGATCCGGGATATCGCTGCTCACCCGACCCAC
CGCGGGCACGTTGTATGTCTCGACCGAGCTCGGCATATTCCGCTCCACAGACTCGGGCACGACCTTTGGCCCAAGTCTCCAC
CGCCCTGACCAACACCTACCAGATCGCCCTGGGTGTGGGCTCAGGCTCGAACTGGAACCTGTATGCCCTTCGGCACCGGCC

Figure 1-B

T. reesei *egl6* nucleotide sequence

GTCAGGGGCTGCCTCTACGCCAGTGGAGACAGCGGCGCCTCCTGGACGGACATCCAGGGCTCCAGGGCTTCGGCTCCAT
CGACAGCAACCAAGTCCCGGAGCGGAGCACCGCGGCAAGTCTACGTGGCACCAACGGCCGGCGTCTTTTACGC
TCAGGGAAACCGTCGGCGGCGCACGGGCGGACTTCCTCGTCGACCAAGCAGAGCAGCAGTACCTCTTCCGCCAGCTC
GAGCACCAACGCTGAGTCGAGCGTTGTATCCACGACCCGGGCTTCGACGGTGACTTCGTCCGAGCACAGCTCGGCCCGCGG
TCCACAGGGGTCAGGGGTCGCCCGTCAATTATGCTCAGTCCGAGGGATTGGGTGGACGGGGCCGACGACGTGTGTGGCGCC
GTATGTCTGCCAGAAAGCAGAAATGATTATTACTACAGTGTGTGATGCTTGAAGTCCCAAGCTCACGAGGAGAGCTACAT
ACCCCTAGGCTCGCAGTAAAGAGCTCAAGCATCCGAAGAAAGCACTAGTAGAGATCCAGTCAGATAATTATCCATTGT
TTGAATTAAATGATCTTCTATTGAAAAA

Predicted *T. reesei* eg16 amino acid sequence

MKVSRLALV LGAVIPAHAA FSWKNVKLGG GGFVPGIIF HPKTKGVAYA RTDIGGLYRL NADDSWTAVT
10 20 30 40 50 60 70

DGIADNAGWH NWGIDAVALD PQDDQKVYAA VGMYTNSWDP SNGAIIRSSD RGATWSFTNL PFKVGNMPG
80 90 100 110 120 130 140

RGAGERLAVD PANSNIIYFG ARSGNGLWKS TDGGVTFSKV SSFTATGTYI PDPSDSNGYN SDKQGLMWVT
150 160 170 180 190 200 210

FDSTSSTTGG ATSRIFVGTA DNITASVYVS TNAGSTWSAV PGQPGKYFFH KAKLQPAEKA LYLTYSDGTG
220 230 240 250 260 270 280

PYDGTLSVW RYDIAGGTWK DITPVSGSDL YFGFGLGLD LQKPGTLVVA SLNSWPPDAQ LFRSTDSGTT
290 300 310 320 330 340 350

WSPAWAWASY PTETYYYSIS TPKAPWIKNN FIDVTSESPS DGLIKRLGWM IESLEIDPTD SNHWLYGTGM
360 370 380 390 400 410 420

TIFGGHDLTN WDTRHNVS IQ SLADGIEEFS VQDLASAPGG SELLAAGVDD NGFTFASRND LGTSPQTVWA
430 440 450 460 470 480 490

TPTWATSTSV DYAGNSVKSV VRVGN TAGTQ VAISSDGGAT WSIDYAADTS MNGGTVAISA DGDITLWSTA
500 510 520 530 540 550 560

SSGVQRSQFQ GSFASVSSLP AGAVIASDKK TNSVFYAGSG STFVYSKDTG SSFTRGPKLG SAGTIRDIAA
570 580 590 600 610 620 630

FOOTNOTES

Figure 2-B

Predicted *T. reesei* egl6 amino acid sequence

HPTTAGTLYV	STDVGIFRST	DSGTTFGQVS	TALTNTYQIA	LGVGSGSNWN	LYAFGTGPSG	ARLYASGDSG	
640	650	660	670	680	690	700	
ASWTDIQGSQ	GFGSIDSTKV	AGSGSTAGQV	YVGTNGRGVF	YAQGTVGGGT	GGTSSSTKQS	SSSTSSASSS	
710	720	730	740	750	760	770	
TTLRSSVVST	TRASTVTSSR	TSSAAGPTGS	GVAGHYAQCG	GIGWTGPTQC	VAPYVCQKQN	DYYYQCV	
780	790	800	810	820	830	837	